

Filed on behalf of: Senior Party Genetics Institute, LLC

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UNITED STATES PATENT AND TRADEMARK OFFICE

BEFORE THE BOARD OF PATENT APPEALS
AND INTERFERENCES

Stryker Corporation,
Junior Party,
(Patent 5,266,683,
Inventors: Hermann Oppermann, Engin Ozkaynak, Thangavel Kuberasampath,
David C. Rueger, Roy H.L. Pang),

v.

Genetics Institute, LLC,
Senior Party,
(Application 08/319,831,
Inventors: Rodney M. Hewick, Jack H. Wang,
John M. Wozney, Anthony J. Celeste).

Patent Interference 105,508 (RES)
(Technology Center 1600)

GENETICS INSTITUTE CLEAN COPY OF CLAIMS

1 Pursuant to the Notice Declaring Interference dated October 6, 2006, Paper No. 1, the
2 party Genetics Institute, LLC, submits a clean copy of its involved claims pending as of the time
3 of the declaration of this interference.

4
5
6 Respectfully submitted,

7
8
9 Dated: October 20, 2006

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10
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PATENT INTERFERENCE 105,508 (RES)

Genetics Institute, LLC,
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(Application 08/319,831,
Inventors: Rodney M. Hewick, Jack H. Wang,
John M. Wozney, Anthony J. Celeste).

CLEAN COPY OF CLAIMS

1. A purified BMP-8 protein characterized by:

(a) at least one of the following sequences:

- i) Arg-His-Glu-Leu-Tyr-Val-Ser-Phe-Gln-Asp-Leu-Gly-Trp-Leu-Asp-Trp-Val-Ile-Ala-Pro-Gln-Gly-Tyr (SEQ ID NO: 1);
- ii) Leu-Ser-Ala-Thr-Ser-Val-Leu-Tyr-Tyr-Asp-Ser-Ser-Asn-Asn-Val-Ile-Leu-Arg (SEQ ID NO: 2); and
- iii) Ala-Cys-Cys-Ala-Pro-Thr-Lys (SEQ ID NO:3);

(b) a molecular weight of 28,000 - 38,000 daltons as determined by sodium dodecyl sulfate polyacrylamide gel electrophoresis; and

(c) a molecular weight of 14,000 - 20,000 daltons under reducing conditions as determined by sodium dodecyl sulfate polyacrylamide gel electrophoresis said protein being a disulfide linked dimer wherein each of the subunits contains the sequences set forth in part (a) and said protein having the ability to induce the formation of cartilage and/or bone.

26. A pharmaceutical formulation for bone and/or cartilage formation comprising an effective amount of a BMP-8 protein of claim 1 in a pharmaceutically acceptable vehicle.

27. A composition of claim 26 further comprising a matrix for supporting said composition and providing a surface for bone and/or cartilage formation.

28. The composition of claim 27 wherein said matrix comprises a material selected from the group consisting of hydroxyapatite, collagen, polylactic acid and tricalcium phosphate.

29. A pharmaceutical composition for wound healing and tissue repair said composition comprising an effective amount of a BMP-8 protein of claim 1 in a pharmaceutically acceptable vehicle.

1 **CERTIFICATE OF SERVICE**

2 I hereby certify that a copy of the foregoing was served on the party Stryker Corporation
3 through its attorney of record on this the 20th day of October, 2006 as follows:
4

5 **VIA FEDERAL EXPRESS**

6 Kilpatrick & Lockhart Nicholson Graham LLP
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10 Respectfully submitted,

11 By: / Kenneth J. Meyers /
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Paper No. _____

UNITED STATES PATENT AND TRADEMARK OFFICE

BEFORE THE BOARD OF PATENT APPEALS
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STRYKER CORPORATION,
Junior Party
(Patent 5,266,683,
Inventors: Hermann Oppermann, Engin Ozkaynak, Thangavel Kuberasampath,
David C. Rueger, Roy H.L. Pang),

v.

GENETICS INSTITUTE, LLC,
Senior Party
(Application 08/319,831,
Inventors: Rodney M. Hewick, Jack H. Wang,
John M. Wozney, Anthony J. Celeste).

Patent Interference No. 105,508 (RES)
(Technology Center 1600)

STRYKER CORPORATION'S CLEAN COPY OF CLAIMS AND SEQUENCES

STRYKER CORPORATION'S CLEAN COPY OF CLAIMS AND SEQUENCES

1 Pursuant to Bd. R. 110(a), Junior Party Stryker Corporation ("Stryker") submits the
2 following clean copy of its involved claims of U.S. Patent 5,266,683. Junior Party Stryker also
3 submits herewith a clean copy of the sequences recited in the involved claims.

- 1 21. An isolated protein comprising the amino acid sequence described by residues
2 306 to 402 of Seq. ID No. 28.
- 3
- 4 22. The protein of claim 21 comprising the amino acid sequence described by
5 residues 270-402 of Seq. ID No. 28 (hOP2-Arg).
- 6
- 7 23. The protein of claim 22 comprising the amino acid sequence described by
8 residues 267 to 402 of Seq. ID No. 28 (hOP2-Pro).
- 9
- 10 24. The protein of claim 23 comprising the amino acid sequence described by
11 residues 264 to 402 of Seq. ID No. 28 (hOP2-Ala).
- 12
- 13 25. The protein of claim 24 comprising the amino acid sequence described by
14 residues 243 to 402 of Seq. ID No. 28 (hOP2-Ser).
- 15
- 16 26. The protein of claim 25 comprising the amino acid sequence described by
17 residues 1 to 402 of Seq. ID No. 28 (hOP2-PP).
- 18
- 19 27. The protein of claim 6, 15, 18 or 21 capable of inducing cartilage and bone
20 formation when implanted in a mammal in association with a matrix.
- 21
- 22 28. Osteogenic protein expressed from recombinant DNA in a host cell,
23 the protein comprising a pair of oxidized subunits disulfide bonded to
24 produce a dimeric species, one of said subunits having an amino acid sequence
25 sufficiently duplicative of the sequence comprising residues 335 to 431 of Seq. ID
26 No. 1 (OPS),
27 such that the disulfide bonded dimeric species comprising said subunit has
28 a conformation capable of inducing cartilage and endochondral bone formation in
29 a mammal when disposed within a matrix implanted in said mammal.
- 30
- 31 29. Osteogenic protein expressed from recombinant DNA in a host cell,

1 the protein comprising a pair of oxidized subunits disulfide bonded to
2 produce a dimeric species, having a conformation capable of inducing cartilage
3 and endochondral bone formation in a mammal when disposed within a matrix
4 implanted in said mammal,

5 one of said subunits having an amino acid sequence encoded by a nucleic
6 acid capable of hybridizing to a nucleic acid encoding OPS (res. 335-431, Seq. ID
7 No. 1) under stringent hybridization conditions.
8

9 39. The protein of claim 28 or 29 wherein said subunit comprises at least the
10 osteogenically active region of a protein selected from the group consisting of:
11 mOP1-PP (residues 1-430, Seq. ID No. 24); mOP2-PP (residues 1-399 of Seq. ID
12 No. 26); and hOP2-PP (residues 1-402 of Seq. ID No. 28).
13

14 45. An isolated polypeptide chain useful as a subunit of a dimeric osteogenic protein,
15 said polypeptide chain having an amino acid sequence sharing greater than 74%
16 identity with the sequence described by residues 264-402 of Seq. ID No. 28
17 (hOP2-Ala) such that the disulfide bonded dimeric species comprising said
18 polypeptide chain is capable of inducing endochondral bone formation when
19 implanted in a mammal in association with a matrix.
20

21 46. An isolated polypeptide chain useful as a subunit of a dimeric osteogenic protein
22 having a conformation capable of inducing endochondral bone formation in a
23 mammal when implanted in a mammal in association with a matrix,
24 said polypeptide chain having an amino acid sequence encoded by a
25 nucleic acid capable of hybridizing to a nucleic acid encoding the pro region of
26 mOP2-PP (res. 17-260 of Seq. ID No. 26) or hOP2-PP (res. 17-263 of Seq. ID
27 No. 28) under stringent hybridization conditions.
28

29 47. The polypeptide chain of claim 45 or 46 having an amino acid sequence sharing
30 greater than 80% identity with the amino acid sequence of hOP2-Ala.
31

1 48. The polypeptide chain of claim 47 having an amino acid sequence sharing greater
2 than 85% identity with the amino acid sequence of hOP2-Ala.

3
4 49. The polypeptide chain of claim 45 or 46 wherein said amino acid sequence is
5 selected from the group consisting of: mOP2-Ala (residues 261-399 Seq. ID No.
6 26); hOP2-Ala (residues 264-402 of Seq. ID No. 28); hOP2-Pro (residues 267-
7 402 of Seq. ID No. 28); hOP2-Arg (residues 270-402 of Seq. ID No. 28) and
8 hOP2-Ser (residues 243-402 of Seq. ID No. 28).

9
10 50. The polypeptide chain of claim 45 or 46 wherein said amino acid sequence is
11 derived from an amino acid sequence selected from the group consisting of:
12 mOP2-PP (residues 1-399 of Seq. ID No. 26) and hOP2-PP (residues 1-402 of
13 Seq. ID No. 28) including allelic variants thereof, and natural and biosynthetic
14 mutants thereof.

15
16 51. The polypeptide chain of claim 45 or 46 that is glycosylated.

17
18 52. An isolated dimeric protein capable of inducing cartilage or endochondral bone
19 formation in a mammal when implanted in said mammal in association with a
20 matrix,

21 said protein comprising a pair of disulfide-bonded polypeptide chains
22 constituting a dimeric species, wherein each said polypeptide chain is the
23 polypeptide chain of claim 45 or 46.

24
25 53. The dimeric protein of claim 52 wherein each said polypeptide chain is
26 independently selected and comprises at least the osteogenically active region of
27 mOP2-PP (residues 1-399 of Seq. ID No. 26) or hOP2-PP (residues 1-402 of Seq.
28 ID No. 28).

29
30 54. The dimeric protein of claim 53, wherein each said polypeptide chain is
31 independently selected from the group consisting of: mOP2-Ala (residues 261-
32 399 Seq. ID No. 26); hOP2-Ala (residues 264-402 of Seq. ID No. 28); hOP2-Pro

(residues 267-402 of Seq. ID No. 28); hOP2-Arg (residues 270-402 of Seq. ID No. 28) and hOP2-Ser (residues 243-402 of Seq. ID No. 28).

58. A protein expressed from recombinant DNA in a host cell, said protein comprising an amino acid sequence encoded by a nucleic acid capable of hybridizing to a nucleic acid encoding residues 306-402 of hOP2 (Seq. ID No. 28) under stringent hybridization conditions.

Interference No. 105,508 (RES)
STRYKER CORPORATION v. GENETICS INSTITUTE, LLC

SEQUENCE DESCRIPTION: SEQ ID NO:1:

5	GGTGCGGGCC CGGAGCCCGG AGCCCGGGTA GCGCGTAGAG CCGGCGCG ATG CAC GTG	57
6	Met His Val	
7	1	
9	CGC TCA CTG CGA GCT GCG GCG CCG CAC AGC TTC GTG GCG CTC TGG GCA	105
10	Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala	
11	5 10 15	
13	CCC CTG TTC CTG CTG CGC TCC GCC CTG GCC GAC TTC AGC CTG GAC AAC	153
14	Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn	
15	20 25 30 35	
17	GAG GTG CAC TCG AGC TTC ATC CAC CGG CGC CTC CGC AGC CAG GAG CGG	201
18	Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser Gln Glu Arg	
19	40 45 50	
21	CGG GAG ATG CAG CGC GAG ATC CTC TCC ATT TTG GGC TTG CCC CAC CGC	249
22	Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg	
23	55 60 65	
25	CCG CGC CCG CAC CTC CAG GGC AAG CAC AAC TCG GCA CCC ATG TTC ATG	297
26	Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro Met Phe Met	
27	70 75 80	
29	CTG GAC CTG TAC AAC GCC ATG GCG GTG GAG GAG GGC GGC GGG CCC GGC	345
30	Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly Gly Pro Gly	
31	85 90 95	
33	GGC CAG GGC TTC TCC TAC CCC TAC AAG GCC GTC TTC AGT ACC CAG GGC	393
34	Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser Thr Gln Gly	
35	100 105 110 115	
37	CCC CCT CTG GCC AGC CTG CAA GAT AGC CAT TTC CTC ACC GAC GCC GAC	441
38	Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr Asp Ala Asp	
39	120 125 130	
41	ATG GTC ATG AGC TTC GTC AAC CTC GTG GAA CAT GAC AAG GAA TTC TTC	489
42	Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys Glu Phe Phe	
43	135 140 145	
45	CAC CCA CGC TAC CAC CAT CGA GAG TTC CGG TTT GAT CTT TCC AAG ATC	537
46	His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu Ser Lys Ile	
47	150 155 160	
49	CCA GAA GGG GAA GCT GTC ACG GCA GCC GAA TTC CGG ATC TAC AAG GAC	585
50	Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Asp	
51	165 170 175	
53	TAC ATC CGG GAA CGC TTC GAC AAT GAG ACG TTC CGG ATC AGC GTT TAT	633
54	Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile Ser Val Tyr	
55	180 185 190 195	
57	CAG GTG CTC CAG GAG CAC TTG GGC AGG GAA TCG GAT CTC TTC CTG CTC	681

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1	Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu Phe Leu Leu	
2	200 205 210	
3		
4	GAC AGC CGT ACC CTC TGG GCC TCG GAG GAG GGC TGG CTG GTG TTT GAC	729
5	Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu Val Phe Asp	
6	215 220 225	
7		
8	ATC ACA GCC ACC AGC AAC CAC TGG GTG GTC AAT CCG CGG CAC AAC CTG	777
9	Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg His Asn Leu	
10	230 235 240	
11		
12	GGC CTG CAG CTC TCG GTG GAG ACG CTG GAT GGG CAG AGC ATC AAC CCC	825
13	Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser Ile Asn Pro	
14	245 250 255	
15		
16	AAG TTG GCG GGC CTG ATT GGG CGG CAC GGG CCC CAG AAC AAG CAG CCC	873
17	Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn Lys Gln Pro	
18	260 265 270 275	
19		
20	TTC ATG GTG GCT TTC TTC AAG GCC ACG GAG GTC CAC TTC CGC AGC ATC	921
21	Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe Arg Ser Ile	
22	280 285 290	
23		
24	CGG TCC ACG GGG AGC AAA CAG CGC AGC CAG AAC CGC TCC AAG ACG CCC	969
25	Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro	
26	295 300 305	
27		
28	AAG AAC CAG GAA GCC CTG CGG ATG GCC AAC GTG GCA GAG AAC AGC AGC	1017
29	Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu Asn Ser Ser	
30	310 315 320	
31		
32	AGC GAC CAG AGG CAG GCC TGT AAG AAG CAC GAG CTG TAT GTC AGC TTC	1065
33	Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe	
34	325 330 335	
35		
36	CGA GAC CTG GGC TGG CAG GAC TGG ATC ATC GCG CCT GAA GGC TAC GCC	1113
37	Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala	
38	340 345 350 355	
39		
40	GCC TAC TAC TGT GAG GGG GAG TGT GCC TTC CCT CTG AAC TCC TAC ATG	1161
41	Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met	
42	360 365 370	
43		
44	AAC GCC ACC AAC CAC GCC ATC GTG CAG ACG CTG GTC CAC TTC ATC AAC	1209
45	Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn	
46	375 380 385	
47		
48	CCG GAA ACG GTG CCC AAG CCC TGC TGT GCG CCC ACG CAG CTC AAT GCC	1257
49	Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala	
50	390 395 400	
51		
52	ATC TCC GTC CTC TAC TTC GAT GAC AGC TCC AAC GTC ATC CTG AAG AAA	1305
53	Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys	
54	405 410 415	
55		
56	TAC AGA AAC ATG GTG GTC CGG GCC TGT GGC TGC CAC TAGCTCCTCC	1351
57	Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His	
58	420 425 430	

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	120	125	130	
1				
2				
3	ATG AGC TTC GTC AAC CTA GTG GAA CAT GAC AAA GAA TTC TTC CAC CCT			547
4	Met Ser Phe Val Asn Leu Val Glu His Asp Lys Glu Phe Phe His Pro			
5	135	140	145	
6				
7	CGA TAC CAC CAT CGG GAG TTC CGG TTT GAT CTT TCC AAG ATC CCC GAG			595
8	Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu Ser Lys Ile Pro Glu			
9	150	155	160	
10				
11	GGC GAA CGG GTG ACC GCA GCC GAA TTC AGG ATC TAT AAG GAC TAC ATC			643
12	Gly Glu Arg Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Asp Tyr Ile			
13	165	170	175	180
14				
15	CGG GAG CGA TTT GAC AAC GAG ACC TTC CAG ATC ACA GTC TAT CAG GTG			691
16	Arg Glu Arg Phe Asp Asn Glu Thr Phe Gln Ile Thr Val Tyr Gln Val			
17	185	190	195	
18				
19	CTC CAG GAG CAC TCA GGC AGG GAG TCG GAC CTC TTC TTG CTG GAC AGC			739
20	Leu Gln Glu His Ser Gly Arg Glu Ser Asp Leu Phe Leu Leu Asp Ser			
21	200	205	210	
22				
23	CGC ACC ATC TGG GCT TCT GAG GAG GGC TGG TTG GTG TTT GAT ATC ACA			787
24	Arg Thr Ile Trp Ala Ser Glu Glu Gly Trp Leu Val Phe Asp Ile Thr			
25	215	220	225	
26				
27	GCC ACC AGC AAC CAC TGG GTG GTC AAC CCT CGG CAC AAC CTG GGC TTA			835
28	Ala Thr Ser Asn His Trp Val Val Asn Pro Arg His Asn Leu Gly Leu			
29	230	235	240	
30				
31	CAG CTC TCT GTG GAG ACC CTG GAT GGG CAG AGC ATC AAC CCC AAG TTG			883
32	Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser Ile Asn Pro Lys Leu			
33	245	250	255	260
34				
35	GCA GGC CTG ATT GGA CGG CAT GGA CCC CAG AAC AAG CAA CCC TTC ATG			931
36	Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn Lys Gln Pro Phe Met			
37	265	270	275	
38				
39	GTG GCC TTC TTC AAG GCC ACG GAA GTC CAT CTC CGT AGT ATC CGG TCC			979
40	Val Ala Phe Phe Lys Ala Thr Glu Val His Leu Arg Ser Ile Arg Ser			
41	280	285	290	
42				
43	ACG GGG GGC AAG CAG CGC AGC CAG AAT CGC TCC AAG ACG CCA AAG AAC			1027
44	Thr Gly Gly Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro Lys Asn			
45	295	300	305	
46				
47	CAA GAG GCC CTG AGG ATG GCC AGT GTG GCA GAA AAC AGC AGC AGT GAC			1075
48	Gln Glu Ala Leu Arg Met Ala Ser Val Ala Glu Asn Ser Ser Ser Asp			
49	310	315	320	
50				
51	CAG AGG CAG GCC TGC AAG AAA CAT GAG CTG TAC GTC AGC TTC CGA GAC			1123
52	Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg Asp			
53	325	330	335	340
54				
55	CTT GGC TGG CAG GAC TGG ATC ATT GCA CCT GAA GGC TAT GCT GCC TAC			1171
56	Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala Tyr			
57	345	350	355	
58				

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1	TAC TGT GAG GGA GAG TGC GCC TTC CCT CTG AAC TCC TAC ATG AAC GCC	1219
2	Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn Ala	
3	360 365 370	
4		
5	ACC AAC CAC GCC ATC GTC CAG ACA CTG GTT CAC TTC ATC AAC CCA GAC	1267
6	Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn Pro Asp	
7	375 380 385	
8		
9	ACA GTA CCC AAG CCC TGC TGT GCG CCC ACC CAG CTC AAC GCC ATC TCT	1315
10	Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala Ile Ser	
11	390 395 400	
12		
13	GTC CTC TAC TTC GAC GAC AGC TCT AAT GTC ATC CTG AAG AAG TAC AGA	1363
14	Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg	
15	405 410 415 420	
16		
17	AAC ATG GTG GTC CGG GCC TGT GGC TGC CAC TAGCTCTTCC TGAGACCCTG	1413
18	Asn Met Val Val Arg Ala Cys Gly Cys His	
19	425 430	
20		
21	ACCTTTGCGG GGCCACACCT TTCCAAATCT TCGATGTCTC ACCATCTAAG TCTCTCACTG	1473
22		
23	CCCACCTTGG CGAGGAGAAC AGACCAACCT CTCCTGAGCC TTCCCTCACC TCCCAACCGG	1533
24		
25	AAGCATGTAA GGGTTCCAGA AACCTGAGCG TGCAGCAGCT GATGAGCGCC CTTTCCTTCT	1593
26		
27	GGCACGTGAC GGACAAGATC CTACCAGCTA CCACAGCAAA CGCCTAAGAG CAGGAAAAAT	1653
28		
29	GTCTGCCAGG AAAGTGTCCA GTGTCCACAT GGCCCCCTGGC GCTCTGAGTC TTTGAGGAGT	1713
30		
31	AATCGCAAGC CTCGTTTCAGC TGCAGCAGAA GGAAGGGCTT AGCCAGGGTG GCGGCTGGCG	1773
32		
33	TCTGTGTTGA AGGGAAACCA AGCAGAAGCC ACTGTAATGA TATGTCACAA TAAAACCCAT	1833
34		
35	GAATGAAAAA AAAAAAAAAA AAAAAAAAAA AAAAGAATTC	1873
36		
37		
38		
39		
40	SEQUENCE DESCRIPTION: SEQ ID NO:26:	
41		
42	gaattccgct gccaggcaca ggtgcgcgct ctggtcctcc ccgtctggcg tcagccgagc	60
43		
44	ccgaccagct accagtggat gcgcgcgcgc tgaaagtccg ag atg gct atg cgt	114
45	Met Ala Met Arg	
46	1	
47		
48	ccc ggg cca ctc tgg cta ttg ggc ctt gct ctg tgc gcg ctg gga ggc	162
49	Pro Gly Pro Leu Trp Leu Leu Gly Leu Ala Leu Cys Ala Leu Gly Gly	
50	5 10 15 20	
51		
52	ggc cac ggt ccc ggt ccc ccg cac acc tgt ccc cag cgt cgc ctg gga	210
53	Gly His Gly Pro Gly Pro Pro His Thr Cys Pro Gln Arg Arg Leu Gly	
54	25 30 35	
55		
56	gcg cgc gac cgg gac atg cag cgt gaa atc ctg ccg gtg ctc ggg cta	258
57	Ala Arg Asp Arg Asp Met Gln Arg Glu Ile Leu Pro Val Leu Gly Leu	
58	40 45 50	

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1	Pro Asn Lys Leu Pro Gly Ile Phe Asp Asp Gly His Gly Ser Arg Gly	
2	280 285 290	
3		
4	aga gag gtt tgc cgc agg cat gag ctc tac gtc aga ttc cgt gac ctt	1026
5	Arg Glu Val Cys Arg Arg His Glu Leu Tyr Val Arg Phe Arg Asp Leu	
6	295 300 305	
7		
8	ggc tgg ctg gac tgg gtc atc gcc ccc cag ggc tac tct gcc tat tac	1074
9	Gly Trp Leu Asp Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala Tyr Tyr	
10	310 315 320	
11		
12	tgt gag ggg gag tgt gct ttc cca ctg gac tcc tgt atg aac gcc acc	1122
13	Cys Glu Gly Glu Cys Ala Phe Pro Leu Asp Ser Cys Met Asn Ala Thr	
14	325 330 335 340	
15		
16	aac cat gcc atc ttg cag tct ctg gtg cac ctg atg aag cca gat gtt	1170
17	Asn His Ala Ile Leu Gln Ser Leu Val His Leu Met Lys Pro Asp Val	
18	345 350 355	
19		
20	gtc ccc aag gca tgc tgt gca ccc acc aaa ctg agt gcc acc tct gtg	1218
21	Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr Ser Val	
22	360 365 370	
23		
24	ctg tac tat gac agc agc aac aat gtc atc ctg cgt aaa cac cgt aac	1266
25	Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His Arg Asn	
26	375 380 385	
27		
28	atg gtg gtc aag gcc tgt ggc tgc cac tgaggcccg cccagcatcc	1313
29	Met Val Val Lys Ala Cys Gly Cys His	
30	390 395	
31		
32	tgttttact accttaccat ctggccgggc cctctctccag aggcagaaac ctttctatgt	1373
33		
34	tatcatagct cagacagggg caatgggagg cccttcactt cccctggcca ctctctgcta	1433
35		
36	aaattctggt ctttcccagt tctctgtgcc ttcatggggt ttcggggcta tcaccccgcc	1493
37		
38	ctctccatcc tctacccca agcatagact gaatgcacac agcatcccag agctatgcta	1553
39		
40	actgagaggt ctgggggtcag cactgaaggc ccacatgagg aagactgac cttggccatc	1613
41		
42	ctcagcccac aatggcaaat tctggatggt ctaagaagcc ctggaattct aaactagatg	1673
43		
44	atctgggctc tctgcaccat tcattgtggc agttgggaca tttttaggta taacagacac	1733
45		
46	atacacttag atcaatgcat cgctgtactc cttgaaatca gagctagctt gttagaaaaa	1793
47		
48	gaatcagagc caggtatagc ggtgcatgtc attaatccca gcgctaaaga gacagagaca	1853
49		
50	ggagaatctc tgtgagttca aggccacata gaaagagcct gtctcgggag caggaaaaaa	1913
51		
52	aaaaaaaaacg gaattc	1929
53		
54		
55		
56		
57	SEQUENCE DESCRIPTION: SEQ ID NO:28:	
58		

STRYKER CORPORATION v. GENETICS INSTITUTE, LLC

1	GGCGCCGGCA GAGCAGGAGT GGCTGGAGGA GCTGTGGTTG GAGCAGGAGG TGGCACGGCA	60
2		
3	GGGCTGGAGG GCTCCCTATG AGTGGCGGAG ACGGCCAGG AGGCGCTGGA GCAACAGCTC	120
4		
5	CCACACCGCA CCAAGCGGTG GCTGCAGGAG CTCGCCCATC GCCCCTGCGC TGCTCGGACC	180
6		
7	GCGGCCACAG CCGGACTGGC GGGTACGGCG GCGACAGAGG CATTGGCCGA GAGTCCCAGT	240
8		
9	CCGCAGAGTA GCCCCGGCCT CGAGGCGGTG GCGTCCCGGT CCTCTCCGTC CAGGAGCCAG	300
10		
11	GACAGGTGTC GCGCGGCGGG GCTCCAGGGA CCGCGCCTGA GGCCGGCTGC CCGCCCGTCC	360
12		
13	CGCCCCGCCC CGCCGCCCCG CGCCGCGCGA GCCCAGCCTC CTTGCCGTCG GGGCGTCCCC	420
14		
15	AGGCCCTGGG TCGGCCGCGG AGCCGATGCG CGCCCGCTGA GCGCCCCAGC TGAGCGCCCC	480
16		
17	CGGCCTGCC ATG ACC GCG CTC CCC GGC CCG CTC TGG CTC CTG GGC CTG	528
18	Met Thr Ala Leu Pro Gly Pro Leu Trp Leu Leu Gly Leu	
19	1 5 10	
20		
21	GCG CTA TGC GCG CTG GGC GGG GGC GGC CCC GGC CTG CGA CCC CCG CCC	576
22	Ala Leu Cys Ala Leu Gly Gly Gly Gly Pro Gly Leu Arg Pro Pro Pro	
23	15 20 25	
24		
25	GGC TGT CCC CAG CGA CGT CTG GGC GCG CGC GAG CGC CGG GAC GTG CAG	624
26	Gly Cys Pro Gln Arg Arg Leu Gly Ala Arg Glu Arg Arg Asp Val Gln	
27	30 35 40 45	
28		
29	CGC GAG ATC CTG GCG GTG CTC GGG CTG CCT GGG CGG CCC CGG CCC CGC	672
30	Arg Glu Ile Leu Ala Val Leu Gly Leu Pro Gly Arg Pro Arg Pro Arg	
31	50 55 60	
32		
33	GCG CCA CCC GCC GCC TCC CGG CTG CCC GCG TCC GCG CCG CTC TTC ATG	720
34	Ala Pro Pro Ala Ala Ser Arg Leu Pro Ala Ser Ala Pro Leu Phe Met	
35	65 70 75	
36		
37	CTG GAC CTG TAC CAC GCC ATG GCC GGC GAC GAC GAC GAG GAC GGC GCG	768
38	Leu Asp Leu Tyr His Ala Met Ala Gly Asp Asp Asp Glu Asp Gly Ala	
39	80 85 90	
40		
41	CCC GCG GAG CGG CGC CTG GGC CGC GCC GAC CTG GTC ATG AGC TTC GTT	816
42	Pro Ala Glu Arg Arg Leu Gly Arg Ala Asp Leu Val Met Ser Phe Val	
43	95 100 105	
44		
45	AAC ATG GTG GAG CGA GAC CGT GCC CTG GGC CAC CAG GAG CCC CAT TGG	864
46	Asn Met Val Glu Arg Asp Arg Ala Leu Gly His Gln Glu Pro His Trp	
47	110 115 120 125	
48		
49	AAG GAG TTC CGC TTT GAC CTG ACC CAG ATC CCG GCT GGG GAG GCG GTC	912
50	Lys Glu Phe Arg Phe Asp Leu Thr Gln Ile Pro Ala Gly Glu Ala Val	
51	130 135 140	
52		
53	ACA GCT GCG GAG TTC CGG ATT TAC AAG GTG CCC AGC ATC CAC CTG CTC	960
54	Thr Ala Ala Glu Phe Arg Ile Tyr Lys Val Pro Ser Ile His Leu Leu	
55	145 150 155	
56		
57	AAC AGG ACC CTC CAC GTC AGC ATG TTC CAG GTG GTC CAG GAG CAG TCC	1008
58	Asn Arg Thr Leu His Val Ser Met Phe Gln Val Val Gln Glu Gln Ser	

1		160		165		170	
2							
3	AAC	AGG	GAG	TCT	GAC	TTG	TTC
4	Asn	Arg	Glu	Ser	Asp	Leu	Phe
5	175					180	
6							
7	GGA	GAC	GAG	GGC	TGG	CTG	GTG
8	Gly	Asp	Glu	Gly	Trp	Leu	Val
9	190					195	
10							
11	TGG	TTG	CTG	AAG	CGT	CAC	AAG
12	Trp	Leu	Leu	Lys	Arg	His	Lys
13							
14							
15	ACT	GAG	GAC	GGG	CAC	AGC	GTG
16	Thr	Glu	Asp	Gly	His	Ser	Val
17							
18							
19	CAA	CGG	GCC	CCA	CGC	TCC	CAA
20	Gln	Arg	Ala	Pro	Arg	Ser	Gln
21	240						
22							
23	GCC	AGT	CCG	AGT	CCC	ATC	CGC
24	Ala	Ser	Pro	Ser	Pro	Ile	Arg
25	255						
26							
27	AGG	AGG	CAG	CCG	AAG	AAA	AGC
28	Arg	Arg	Gln	Pro	Lys	Lys	Ser
29	270						
30							
31	CCA	GGG	ATC	TTT	GAT	GAC	GTC
32	Pro	Gly	Ile	Phe	Asp	Asp	Val
33							
34							
35	CGT	CGG	CAC	GAG	CTC	TAC	GTC
36	Arg	Arg	His	Glu	Leu	Tyr	Val
37							
38							
39	TGG	GTC	ATC	GCT	CCC	CAA	GGC
40	Trp	Val	Ile	Ala	Pro	Gln	Gly
41	320						
42							
43	TGC	TCC	TTC	CCA	CTG	GAC	TCC
44	Cys	Ser	Phe	Pro	Leu	Asp	Ser
45	335						
46							
47	CTG	CAG	TCC	CTG	GTG	CAC	CTG
48	Leu	Gln	Ser	Leu	Val	His	Leu
49	350						
50							
51	TGC	TGT	GCA	CCC	ACC	AAG	CTG
52	Cys	Cys	Ala	Pro	Thr	Lys	Leu
53							
54							
55	AGC	AGC	AAC	AAC	GTC	ATC	CTG
56	Ser	Ser	Asn	Asn	Val	Ile	Leu
57							
58							

Interference No. 105,508 (RES)

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1 GCC TGC GGC TGC CAC T GAGTCAGCCC GCCCAGCCCT ACTGCAG
2 Ala Cys Gly Cys His
3 400

1723

Dated: October 20, 2006

/CONNIE WONG/

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